

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.7349 Seconds

(Without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613b-21

Perfect score: 605
Sequence: 1 MONNATFOQKHIIIMPICN.....ICVKECNOYVPHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR-73:***
1: pirl:***
2: pirl:***
3: pirl:***
4: pirl:***

Pred. Nc. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB, ID	Description
1	582.5	96.3	111	2, A27121	ribonuclease-relat
2	451	74.5	111	1, JX0120	pancreatic ribonuc
3	370	61.2	111	2, JX0085	pancreatic ribonuc
4	270.5	44.7	104	2, A39035	ribonuclease-relat
5	136.5	22.6	145	1, A35932	angiotensin precurs
6	131.5	21.7	124	1, NRMHR	pancreatic ribonuc
7	129.5	21.4	124	1, NRP	pancreatic ribonuc
8	129.5	21.4	167	2, S20066	pancreatic-type r1
9	127.5	21.1	119	2, S41111	pancreatic ribonuc
10	119	19.7	122	1, NRMGR	pancreatic ribonuc
11	118.5	19.6	123	1, A43825	angiotensin - pig
12	118.5	19.6	124	1, NRP	pancreatic ribonuc
13	115.5	19.3	128	1, NRCU	pancreatic ribonuc
14	115.5	19.3	149	1, NRM	pancreatic ribonuc
15	114.5	18.9	123	1, NRCPB	pancreatic ribonuc
16	114	18.8	125	1, A32474	pancreatic ribonuc
17	113.5	18.8	124	1, NRCM	pancreatic ribonuc
18	113.5	18.8	124	1, NRCMB	pancreatic ribonuc
19	113.5	18.8	124	1, NRCMB	pancreatic ribonuc
20	113.5	18.8	128	1, NRCB	pancreatic ribonuc
21	113	18.7	147	1, NRMAG	pancreatic ribonuc
22	112.5	18.6	138	1, NRS	angiotensin precurs
23	110.5	18.3	124	2, S0849	pancreatic ribonuc
24	109.5	18.1	124	1, NRDEN	ribonuclease - dom
25	109	18.0	125	1, B43825	pancreatic ribonuc
26	108.5	17.9	124	1, NRGF	angiotensin - rabbi
27	108.5	17.9	124	1, NRD	pancreatic ribonuc
28	108.5	17.9	130	2, S22608	pancreatic ribonuc
29	107.5	17.8	124	1, NRM	pancreatic ribonuc

30	107.5	17.8	158	2, I61900	eosinophil-derived
31	106.5	17.6	124	1, NROB	pancreatic ribonuc
32	106.5	17.6	124	1, NREN	pancreatic ribonuc
33	106.5	17.6	124	2, S07141	pancreatic ribonuc
34	106.5	17.6	124	2, J05560	pancreatic ribonuc
35	106.5	17.6	150	1, NRO	pancreatic ribonuc
36	105.5	17.4	119	2, JX0115	pancreatic ribonuc
37	105.5	17.4	124	1, NRS	pancreatic ribonuc
38	105.5	17.4	152	1, NRT	pancreatic ribonuc
39	104.5	17.3	124	1, NRCB	pancreatic ribonuc
40	103.5	17.1	125	4, A47498	pancreatic ribonuc
41	103.5	17.1	150	1, NROB	seminal ribonuclease
42	102.5	16.9	124	1, NRP	pancreatic ribonuc
43	101	16.7	125	2, S04503	pancreatic ribonuc
44	100.5	16.6	124	1, NRCN	pancreatic ribonuc
45	100.5	16.6	124	1, NRDE	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121 ribonuclease-related stialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K., Takio, K., Kuwada, M., Nitta, K., Sakakibara, F., Kawachi, H., Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of stialic acid-binding lectin from frog (Rana catesbeian

A:Reference number: A27121; MUID:8729649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match

Best Local Similarity 96.3%; Score 582.5; DB 2; Length 111;

Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 2 QNNATFOQKHIIIMPPII-CNTIIDNNIYIVGGCKRYNPFIISSATVKAICGVNLNV 60

Db 1 ENNATFOQKHIIIMPPIINCNTIMDNNTIYVGGCKRYNPFIISSATVKAICGVNLNV 60

OY 61 LSTTRFOLNCTRTSTTRPCPYSSRTETNYICVKECNOYVPHFAGIGRCP 111

Db 61 LSTTRFOLNCTRTSTTRPCPYSSRTETNYICVKECNOYVPHFAGIGRCP 111

RESULT 2

JX0120 ribonuclease-related stialic acid-binding lectin - Japanese frog

C:Species: Rana japonica (Japanese frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JX0120

R:Kamiya, Y., Oyama, F., Oyama, R., Sakakibara, F., Nitta, K., Kawachi, H., Takayana

J. Biochem. 108, 139-145, 1990

A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A:Reference number: JX0120; MUID:91035319; PMID:2229005

A:Accession: JX0120

A:Molecule type: protein

A:Residues: 1-111 <RAM>

A:Experimental source: egg

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin; pyroglyutamic acid

F:1/Modified site: pyroglyutamic acid (Gln) #status experimental

F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 74.5%; Score 451; DB 1; Length 111;

Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

[illegible]

RESULT 3

C:Pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Onga
J. Biochem. 105, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10.3/104/Active site: His, Lys, His #status predicted
F:19-72.34-82.52-97.94-111/Disulfide bonds: #status predicted

Query Match	61.28;	Score 370;	DB 2;	Length 111;
Best Local Similarity	64.99;	Pred No 1	10-20;	

Matches	72;	Conservative	10;	Mismatches	27;	Indels	2;	Gaps	2;
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[illegible]

RESULT 4

C:Ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos
A:Reference number: A39035; MUID:91093131; PMID:1965896
A:Accession: A39035
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match	Score	DB 2	Length
44.78	270.5	104	

Matches	53;	Conservative	17;	Mismatches	32;	Indels	9;	Gaps	4;
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OY 2 QNNATFEQAKHIINT-PIICNTILDNNIYIVGGCKRVTFFISSATTVAICTGYI-NLN 59
 ::| | | | | : : : | | | | | : |
Db 1 EDWLTQKKHITNTRDVCDDIMSTNLF---HCKDKMTFLYSPEPYAICKGIIASKN 56

Qy 60 VLSTRFQNTCTRTSITPRPCPYSSRTETNYICVCKENQYPVHAGIGRC 110
|||: ||: | ::||| : || |||| |||| ||: |
Db 57 VLTTSFPLSDC---NVTSRPCKKKLKKTSTKFCVTCEQAQPVHEVGVCSC 104

RESULT 5
A35932
angiotensin precursor - mouse

N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932

Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A/Title: Isolation and sequencing of mouse angiotensin DNA
A/Reference number: A35932; MUID:91025023; PMID:2222458

A; Status: not compared with conceptual translation

A;Residues: 1-145 <BON>

C;Genetics:

```

n;
end;
C;Function:

```

A; description: hydrolyzes tRNA, induces vascularization of normal and malignant tissue

F:1-24/Domain: signal sequence #status predicted <SIG>
c/keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid

E:25/Modified site: pyrrolidone carboxyl acid (Gln)

F:37,64,137/Active site: His, Lys, His #status predicted
E:50-104,63-115,81-130/Dissulfide bonds: #status predicted

Query Match 22.68: Score 1365: DB 1: 1e

Query Match	22.68; Score 136.5; DB 1; Length 145;
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Matches	31;	Conservative	11;	Mismatches	28;	Indels	7;	Gaps	3
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34 CKRVNTEISSATTVKAICTG-----VINLNLSTTRQQLNCTRTSITPR-PCPYSSRT 87

Db 63 CKDVNTFIHGKSNKAICGANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPQCQYRASA 121

```
QY      88 ETNYICVKCENQYPVHF 104
          ::: ||| |||
Db      122 GFRHVVIACENGLPVHF 138
```

RESULT 6

pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase 1; RNase A
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: Protein
A:Residues: 1-124 <EMM>
S:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys His #status predicted
E:26,84,40-95,58-110,65-72/Disulfide bonds: #status predicted
E:76/Binding site:carbohydrate (asn) (covalent) (partial) #status experimental

Query match 21.78; Score 131.5; DB 1; Length 124;

Best Local Similarity 32.38, Fied: NO: 4.0e-00;
Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQQKHII-----NTPICNTILDNNIYIVGGQCKRVNTEFISSATTVKAICTGVINLNV 60

Db 8 FÖRÖHMDSGNSPGNNPNYCÑÖMMRR-KMTÖGRCKPVNTFVHESLEDDKAVCS--ÖKNV 63

```

Qy      61 L-----STTRQLNCTRTSTTPRP-CPYSSRIETNYICVKE-NQY-PVHF 104
      | : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 LCKNGRTNCYESNSTWHITDGRQTGSSKYPNCAVKYTSQEKHIIIVACEGNPYVPVHF 120

```

RESULT 7

Db 7 FORQMDHEHSTASSNNCLMMKAR-DMTSGRCPLNTFHEPKSVDAVCHOENVTCK 65
 QY 53 TGVINLVNLTSTRFOLNCTRTSTPRP-CPYSSRTETWICVKENOV-PVHF 104
 Db 66 NGRTNC-YKSNRSLTITNCRTGASKRPNCOYETSLNKLQITVACEGQVYPVHF 118
 RESULT 11
 A43825
 angiotensin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S29833; A43825
 R:Bond, M.D.; Striydom, D.J.; Vallee, B.L.
 Biochim. Biophys. Acta 1162, 177-186, 1993
 A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: disacetime
 A:Reference number: S29833; MUID:93192291; PMID:8448182
 A:Accession: S29834
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-123 <BON>
 A>Note: this sequence was submitted to the Protein Sequence Database, December 1992
 C:Superfamily: pancreatic ribonuclease
 Query Match 19.6%; Score 118.5; DB 1; Length 123;
 Best Local Similarity 39.5%; Pred. No. 9.3e-05;
 Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;
 QY 34 CKRVNFTFISSATYKKAICTG---VINLVNLTSTRFOLNCTRTSTPRP-PCPSSKTE 88
 Db 39 CKRVNFTFHGRNDIKATCNDKNGEPYNNFRSRKSPFOITCKHKGGSNRPPCGYRATAG 98
 QY 89 TNYICVKENOVYPVHF 104
 Db 99 FRTIYVACENGLPVPVHF 114
 RESULT 12
 NRPRH
 pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Antilocapra americana (pronghorn)
 C>Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
 C:Accession: A00813
 R:Beintema, J.J.; Gaaststra, W.; Munnikama, J.
 J. Mol. Evol. 13, 305-316, 1979
 A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
 A:Reference number: A00813; MUID:80075014; PMID:513141
 A:Accession: A00813
 A:Molecule type: protein
 A:Residues: 1-124 <BEI>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12-41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 Query Match 19.6%; Score 118.5; DB 1; Length 124;
 Best Local Similarity 29.9%; Pred. No. 9.4e-05;
 Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;
 QY 5 ATFOAKHIIINPT-----ICNTILDNNTIYVGGCKRVNFTFISSATYKAICT---- 53
 Db 6 AKFEROHIDSNPSSVSSNNYCNOMKMSR-NLTGRCRCPVNTFVHESLADVOAVCSOKNVA 64
 QY 54 ---GVILNVLTSTRFOLNCTRTSTPRP-CPISSKRETYICVKE-NOY-PVHF 104
 Db 65 CKNGQTCN-YOSTSTMSITDCEGTGSSKYPKCAVKTQAKKHIIYACEGNDYVPVHY 120
 RESULT 13
 NRCU
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)

N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 C:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreat
 A:Reference number: A00612; MUID:77065676; PMID:998996
 A:Accession: A00822
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-128 <VAN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12-41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 19.3%; Score 116.5; DB 1; Length 128;
 Best Local Similarity 30.8%; Pred. No. 0.00015;
 Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;
 QY 7 FOQKHII-----INPTICNTILDNNTIYVGGCKRVNFTFISSATYKAICTGVINLV 60
 Db 8 FERQHDSRGSPSTPNPNYCNEMKMSR-NMTGRCRCPVNTFVHESLADVOAVC---FOKNV 63
 QY 61 L-----STTRFOLNCTRTSTPRP-CPYSSRTETWICVKE-NOY-PVHF 104
 Db 64 LCKNGQTCNYSNMMHITDCRVTSNSDYPMCSTRTSOEKSIVYVACGNDYVPVHF 120
 RESULT 14
 NRMS
 pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
 N:Alternate names: RNase 1; RNase A
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 C:Accession: A34090; S22598; A00830
 R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
 Mol. Biol. Evol. 7, 29-44, 1990
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo
 A:Reference number: A34090; MUID:90136034; PMID:2299980
 A:Accession: A34090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-149 <SCH>
 A:Cross-references: GB:M27814; MID:g200762; PIDN:AAA40060.1; PID:g200763
 R:Samuelson, L.C.; Webauer, K.; Howard, G.; Schmid, R.M.; Koepflin, D.; Meisler, M.H.
 Nucleic Acids Res. 19, 6935-6941, 1991
 A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specif.
 A:Reference number: S22598; MUID:92107684; PMID:1840677
 A:Accession: S22598
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <SAN>
 A:Cross-references: EMBL:X60103; MID:g53981; PIDN:CAA42697.1; PID:g53982
 R:Rienstra, J.A.; Beintema, J.J.
 Eur. J. Biochem. 98, 399-408, 1979
 A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
 A:Reference number: A00830; MUID:80024269; PMID:556267
 A:Accession: A00830
 A:Molecule type: protein
 A:Residues: 26-149 <LEN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-149/Product: pancreatic ribonuclease #status predicted <MAT>
 F:37,66,144/Active site: His, Lys, His #status predicted
 F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
 F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 19.3%; Score 116.5; DB 1; Length 149;
 Best Local Similarity 29.9%; Pred. No. 0.00018;
 Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;

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OY 7 FOQKH-----INPILCNITLDNNIYVGQCKRVNFIISATVKAICTGVINLV 60
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 33 FORGHMDPSSINSPTICNOMMKRR-DMTNGSCPKPVNTFVHEPLADYQAVCS---QENV 88
   ||::||::||::||::||::||::||::||::||::||::||::||::||
OY 61 L-----STRFOINTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
   ||::||::||::||::||::||::||::||::||::||::||::||::||
DB 89 TCKNRKSNCKYKSSALHTDCHLKGNSKYPNCDYKTYOKKHIIYACEGNPYVPVHF 145
   ||::||::||::||::||::||::||::||::||::||::||::||::||

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RESULT 15

NRGPR

pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)

N:Alternate names: RNase IB

C:Species: *Cavia porcellus* (guinea pig)

C>Date: 24-Apr-1981 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A00823

R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Belintema, J.J.

Eur. J. Biochem. 73, 91-100, 1977

A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a

A:Reference number: A91247; MUID:77185023; PMID:862624

A:Accession: A00826

A:Molecule type: protein

A:Residues: 1-128 <VAM>

A>Note: 64-Pro was also found

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted

F:21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:26-84,40-95,58-110,65+72/disulfide bonds: #status predicted

Query Match

18.9%; Score 114.5; DB 1; Length 128;

Best Local Similarity 30.8%; Pred. No. 0.00024;

Matches 36; Conservative 15; Mismatches 43; Indels 23; Gaps 6;

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OY 7 FOQKH-----INPILCNITLDNNIYVGQCKRVNFIISATVKAICTGVINLV 60
   ||::||::||::||::||::||::||::||::||::||::||::||::||
DB 8 FORGHMDPSSINSPTICNOMMKRR-DMTNGSCPKPVNTFVHEPLADYQAVC---FOKNV 63
   ||::||::||::||::||::||::||::||::||::||::||::||::||
OY 61 L-----STRFOINTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
   ||::||::||::||::||::||::||::||::||::||::||::||::||
DB 64 LCKNGQTNCTQSYSRMRTDCRVTSSSKFPNCSYRMSOAKSIIVACEGDPYVPVHF 120
   ||::||::||::||::||::||::||::||::||::||::||::||::||

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Search completed: June 25, 2003, 14:58:06
 Job time : 13.7349 secs

